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## Erratum to: Detection and sequence/ structure mapping of biophysical constraints to protein variation in saturated mutational libraries and protein sequence alignments with a dedicated server

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## **Erratum**

After publication of the original article [1] it was brought to our attention that the caption to Figure 3 contained a twice recurring error.

The caption reads: "Comparative analyses of deep sequencing data on two closely related HIV RNP variants. a Pie charts summarizing how frequently was each amino acid descriptor picked as the best one for sites in RNP from HIV strains 1934 and 1968. b Sites shaped by isoelectric point with positive (blue) and negative (red) trends in the data for strain 1968 (PDB ID 2IQH [67])".

This should instead read: "Comparative analyses of deep sequencing data on two closely related influenza RNP variants. a Pie charts summarizing how frequently was each amino acid descriptor picked as the best one for sites in RNP from influenza strains 1934 and 1968. b Sites shaped by isoelectric point with positive (blue) and negative (red) trends in the data for strain 1968 (PDB ID 2IQH [67])".

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## Reference

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